RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/ 750, 986 A*

Source: *OIPE*

Date Processed by STIC: *5-23-01*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>**ERROR DETECTED**</u>　　<u>**SUGGESTED CORRECTION**</u>　　　　**SERIAL NUMBER:** *09/750, 986 A*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics　The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
　　　Wrapped Aminos ·　was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
　　　　　　　　　　　　prevent "wrapping."

2____Invalid Line Length　The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino　The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
　　　Numbering　　　　use space characters, instead.

4____Non-ASCII　　　The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
　　　　　　　　　　ensure your subsequent submission is saved in ASCII text.

5____Variable Length　　Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
　　　　　　　　　　　each n or Xaa can only represent a single residue. Please present the maximum number of each
　　　　　　　　　　　residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0　　A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
　　　"bug"　　　　sequences(s) _____. Normally, PatentIn would automatically generate this section from the
　　　　　　　　　　previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
　　　　　　　　　　the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
　　　　　　　　　　Artificial or Unknown sequences.

7____Skipped Sequences　Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
　　　(OLD RULES)　　(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
　　　　　　　　　　　(i)　　　SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
　　　　　　　　　　　(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
　　　　　　　　　　　This sequence is intentionally skipped

　　　　　　　　　　　Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences　Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
　　　(NEW RULES)　　<210> sequence id number
　　　　　　　　　　<400> sequence id number
　　　　　　　　　　000

9____Use of n's or Xaa's　Use of n's and/or Xaa's have been detected in the Sequence Listing.
　　　(NEW RULES)　　Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
　　　　　　　　　　In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ✓ Invalid <213>　　Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
　　　Response　　　scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
　　　　　　　　　　is Artificial Sequence

11____Use of <220>　　Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
　　　　　　　　　　Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
　　　　　　　　　　"Unknown." Please explain source of genetic material in <220> to <223> section.
　　　　　　　　　　(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)　(Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0　　Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
　　　"bug"　　　　resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
　　　　　　　　　　listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

OIPE

RAW SEQUENCE LISTING   DATE: 05/23/2001
PATENT APPLICATION: US/09/750,986A   TIME: 12:37:52

Input Set : A:\B-99982.txt
Output Set: C:\CRF3\05232001\I750986A.raw

ENTERED

see p. 5

Does Not Comply
Corrected Diskette Needed

p. 6.

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 3 <110> APPLICANT: Steinbuchel, Alexander
 4         Priefert, Horst
 5         Rabenhorst, Jurgen
 7 <120> TITLE OF INVENTION: SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL
 8         ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND
 9         VANILLIC ACID AND THEIR USE
11 <130> FILE REFERENCE: Bayer-9998.2-HCL
13 <140> CURRENT APPLICATION NUMBER: 09/750,986A
14 <141> CURRENT FILING DATE: 2000-12-28
16 <150> PRIOR APPLICATION NUMBER: 196 49 655.1 GERMANY
17 <151> PRIOR FILING DATE: 1996-11-29
19 <160> NUMBER OF SEQ ID NOS: 45
21 <170> SOFTWARE: PatentIn Ver. 2.1
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24 <211> LENGTH: 32679
25 <212> TYPE: DNA
26 <213> ORGANISM: Pseudomonas sp.
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (3146)..(3997)
31 <223> OTHER INFORMATION: gene = "ORF1"
33 <400> SEQUENCE: 1
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146 tcc gaa att att gcc ctc gtc cgg gat ccg aat aag gcc gga gac ctt    3268
147 Ser Glu Ile Ile Ala Leu Val Arg Asp Pro Asn Lys Ala Gly Asp Leu
148                  30                  35                  40
150 acc gca cgt ggc atc gtg gtg cgc cag gcc gat tac aac cgg ccg gaa    3316
151 Thr Ala Arg Gly Ile Val Val Arg Gln Ala Asp Tyr Asn Arg Pro Glu
152                  45                  50                  55
154 aca ctc cac cgg gcc ctg att ggg gtc aac cgg ttg ctg ttg att tcc    3364
155 Thr Leu His Arg Ala Leu Ile Gly Val Asn Arg Leu Leu Leu Ile Ser
156          60                  65                  70
158 tcc agt gag gtg ggt caa cga act gcg caa cac cgg gca gtg atc gac    3412
159 Ser Ser Glu Val Gly Gln Arg Thr Ala Gln His Arg Ala Val Ile Asp
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162 gct gcg aag caa gaa ggt atc gag ttg ctg gct tat acg agt ctg ctt    3460
163 Ala Ala Lys Gln Glu Gly Ile Glu Leu Leu Ala Tyr Thr Ser Leu Leu
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181 His Gly Val Leu Leu Gly Cys Ala Gln Asp Gly Leu Ile Ala Ser Ala
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351 gcgcgcagca ctcgagtgct gccacaaggg ctggggcgaa tccgtgatca tcggcgtggc 8177
353 gccggcgggg gccgaaatca acacccgtcc gttccacctg gtgaccggtc gcgtctggcg 8237
355 gggttcggcg ttcggtggcg taaagggccg caccgaactg ccgagctacg tggagaaggc 8297
357 acagcagggc gagatcccgc tggacacctt catcactcac accatgggcc tggacgacat 8357
359 caacacggcc ttcgacctga tggacgaagg gaagagcatc cgctctgttg ttcaattgag 8417
361 tcgctagtga agtggggtga ggaaattgga ttaggaggcg gatggttcct gccgcttaac 8477
363 caccttgtcc cagcttctgg ctgagatttc caagattcgg tgaaatttgc catgccgcaa 8537
365 actcttgctg gacggttgag tctgttatcc ggcaccgacg aattaaccct gcttcttcgg 8597
367 ggtggtcggg gcattgagcg tgaagccttg cgggtcgatg ttcaaggtga actggcgctg 8657
369 acgcctcacc cggcggcgct tggctctgcg ttgacccatc cgacaattac tacggattac 8717
371 gccgaggccc tgcttgagtt gatcactcgg ccggcaaccg attgtgcgca agccttggct 8777
373 gagctggagg agcttcaccg tttcgttcat tcgagacttg aggggagta tctctggaat 8837
375 ctgtccatgc ctggcagatt gccggttgat gagcaaatcc cgattgcttg gtatggacca 8897
377 tcaaatccag gcatgttgcg ccacgtttat cgccgtggcc tagctctgcg ttatggcaag 8957
379 cgaatgcaat gcatcgcagg gattcactac aactactcac tgccgccaga gcttttcgct 9017
381 gtcctgacca aggcagaggt cgggtctccc aagttactgg agcgccagtc agcagcttac 9077
383 atgcgccaaa ttcgcaacct tcggcaatac ggttggttgc tggcctactt gttcggcgct 9137
385 tcccccgcca tctgcaagag cttcttgggg ggcgagagag atgagctagc tcgcatgggg 9197
387 ggcgatacgc tttacatgcc ctatgcaacc agcttgcgca tgagtgacat cgggtaccgc 9257
389 aaccgtgcca tggatgatct atctcccagc ctgaatgatc tgggtgccta tattcgcgat 9317
391 atttgccgtg ctcttcacac tcccgatgcc cagtaccagg cgctgggtgt gtttgcacag 9377
393 ggcgagtggc ggcagttaaa cgccaatcta ttgcagttgg atagtgagta ctacgcactg 9437
395 gcgcgaccga agtcagcgcc cgagcggggg gagcgaaacc tggatgctct cgctaggcgt 9497
397 ggagtccagt atgtggagct gcgcgcactg gatctcgatc cattctcccc gttaggcatt 9557
399 ggcctgacct gcgccaagtt cctcgatggc tttttgcttt tctgcttgtt gtctgaggcg 9617
401 ccggttgatg atcgaaatgc ccagcgttca agaccgggaa aatctgagcc tggccggcaa 9677
403 gtacgggcgt cacctggctt aaagctgcat cggaatggtc agtccattct cctcaaggat 9737
405 tgggcgcagg aagtgttgac ggaggttcag gcctgtgtgg aattgctcga cagtgcaaat 9797
407 gggggctcat ctcacgcatt ggcttggtca gcacaggagg aaaaggtgct taatccggat 9857
409 tgtgcgccat cagctcaggt gctcgcagag atacacagac acggtgggag cttcacggca 9917
411 tttggtcgcc aattagctat cgaccatgca aaacacttca gtgcctcctc gcttgaggct 9977
413 ggcgtagcca aagcgcttga cctccaggcg acgtcgtctc tgcgcgagca gcatcaattg 10037
415 gaggccaacg accgtgcgcc attttctgac taccttcagc aattctccct ggctttcggt 10097
417 caatccgtcg gcgcctctcg tgcgcccaac cctaccgcgc acctcatcga tctgacccct 10157
419 cctgtctaag gttgtcgtgg gagcagatcc gtgggccgag cttcctccag ggcctggccg 10217
421 cagcgatcca gttgctaggt ccctatgctc ttgcataggg taaaaattag ttattgtgtt 10277
423 taacgaaacg tctggcatac tggctttagg cacgagcttc cacgccgaag ttgagagcgt 10337
425 catgaacgat ttttcgtgtg gagagacgat gcccgatgcg gtcgacgagg ttcaggtcct 10397
427 aatggcagtg ccggcggcta aacggaacgt gccgtatttt gaggcttgga gcgtggtgaa 10457
429 gcagcttggc tgctccctgg gcctgtcagg atcacgctgt gtcggcagtg acacttcaaa 10517
431 acaagaaggg cattaagatg atgaatgtta attataaggc tgtcggggcg agcctactcc 10577
433 tcgccttcat ctctcaggga gcttgggcag agagccccgc agcctctggc aatacccctg 10637
435 acatttatcg aaagacctgc acctactgcc atgagcctac tgtcaacaat ggccgggtca 10697
437 ttgcccgaag cctcgggccg actctgcgag ggcgccagat ccctccacag tacacggagt 10757
439 acatggtgcg tcatggacgc ggggcaatgc ctgcattctc tgaagcagaa gtgcctccgg 10817
```

```
<210> 3
<211> 1065
<212> DNA
(<213> not required under old rule)  ───>
```
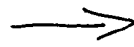
<213> organisms is a mandatory response under the new rules, which is the format you are using.
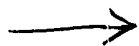
See #10 on the Error Summary sheet.

```
<220>
<221> CDS
<222> (1)..(1062)
<223> product = "Vanillinsaeure-O-Demethylase" / gene =
      "vanA"
```

format you are using.

```
<400> 3
atg ttt ccg aaa aac gcc tgg tat gtc gct tgc act ccg gat gaa atc    48
Met Phe Pro Lys Asn Ala Trp Tyr Val Ala Cys Thr Pro Asp Glu Ile
 1           5                  10                  15
```

Note: This error occurs throughout the sequence listing. Please review and correct all instances.

VERIFICATION SUMMARY   DATE: 05/23/2001
PATENT APPLICATION: US/09/750,986A   TIME: 12:37:53

Input Set : A:\B-99982.txt
Output Set: C:\CRF3\05232001\I750986A.raw

L:4934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:4937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:4955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45